Patent Claims

1. A method of microbial production of amino acids of aspartate and/or glutamate families in which the pyruvate-carboxylase activity is increased by genetic modification of the enzyme and/or the pyruvate-carboxylase gene expression of the corresponding amino-acid-producing micro organism.

2. The method of claim 1, characterized in that, by mutation of the endogenous pyruvate-carboxylase gene an enzyme with higher pyruvate-carboxylase activity is produced.

3. The method of claim 1 ~~or 2~~, characterized in that, the gene expression of the pyruvate-carboxylase is increased by increasing the gene copy number.

4. The method according to claim 3, characterized in that, to increase the gene copy number the pyruvate-carboxylase gene is incorporated in a gene construct.

5. The method according to claim 3, characterized in that, the gene is incorporated in a gene construct which contains regulatory gene sequences associated with the pyruvate-carboxylase gene.

6. The method according to claim 4 ~~or 5~~, characterized in that, the corresponding amino-acid-producing microorganism is transformed with the gene-containing gene construct.

7. The method according to claim 6, characterized in that, a microorganism of the species *Corynebacterium* is transformed with the gene containing the gene construct.

8. The method according to claim 6 ~~or 7~~, characterized in that, for the transformation a microorganism is used in which the enzyme participating in the synthesis of the corresponding amino acid is deregulated and/or wherein an enhanced export carrier activity is shown for the corresponding amino acid.

9. The method according to claim 6 ~~to 8~~, characterized in that, for the transformation a microorganism is used which has a higher proportion of the central metabolism metabolites of the corresponding amino acid participating in the synthesis.

10. The method according to claim 6 ~~to 9~~, characterized in that, for the transformation a microorganism is used in which biosynthesis paths competing with the corresponding amino acid biosynthesis paths runs with reduced activity.

11. The method according to ~~one of the preceding~~ claims 1, characterized in that, the pyruvate-carboxylase gene is isolated from a microorganism strain of the variety *Corynebacterium*.

12. The method according to ~~one of the preceding~~ claims 1, characterized in that, the gene expression is increased by reinforcement of the transcription signal.

13. The method according to ~~one of the preceding~~ claims 1, characterized in that, the pyruvate-carboxylase gene has the tac-promot r ahead of the pyruvate-carboxylase gene.

14. The method according to claim 13, characterized in that, the tac-promoter is associated with regulatory sequences.

15. The method according to ~~one of the preceding~~ claim 1, characterized in that, the pyruvate-carboxylase gene is a gene with the amino acid sequence given under SEQ ID No. 2 and its allele variation coding nucleotide sequences.

16. The method according to claim 15, characterized in that, with the pyruvate-carboxylase gene a gene with the nucleotide sequence of nucleotide 165 to 3587 according to SEQ ID No. 1 or a substantially identically-effective DNA sequence is used.

17. The method according to ~~one of the preceding~~ claim 1, for the production of lysine, threonine, homoserine, glutamate and/or arginine.

18. A pyruvate-carboxylase gene coding for the amino acid sequence given under SEQ ID No. 2 and /or a nucleotide sequence coding for its allele variations.

19. The pyruvate-carboxylase gene according to claim 18 with the nucleotide sequence of nucleotides 165 to 3587 according to SEQ ID No. 1 or a substantially identically-effective DNA sequence.

20. The pyruvate-carboxylase gene according to claim 18 ~~or 19~~ with a preceding promoter of the nucleotide sequence from nucleotide 20 to 109 according to SEQ ID No. 1 or a substantially-identically-effective D NA sequence.

21. The pyruvate-carboxylate gene according to claim 18 ~~or 19~~, with preceding tac-promoter.

22. The pyruvate-carboxylase gene according to claim 21 with the regulatory sequence associated with the promoter.

23. The pyruvate-carboxylase gene according to ~~one of~~ claims 18 ~~to 20~~ with these regulatory gene sequences associated therewith.

24. A gene structure containing a pyruvate-carboxylase gene according to ~~one of~~ claims 18 ~~to 23~~.

25. A vector containing a pyruvate-carboxylase gene ~~according to one of claims 18 to 23~~ or a gene structure according to claim ~~21~~ 18.

26. Transformed cells containing in replicatable form a pyruvate-carboxylase gene ~~according to one of claims 18 to 23~~, or a gene structure according to claim ~~21~~ 18.

27. Transformed cells ~~according to claim 26~~ containing a vector according to claim 25.

28. Transformed cells according to claim 26 ~~or 27~~, characterized in that they belong to the variety *Corynebacterium*.

29. Transformed cells according to ~~one of~~ claims 26 ~~to 28~~, characterized in that, enzymes which participate in the synthesis of the corresponding amino acid and/or enzyme which participate in the export of the corresponding amino acid are deregulated.

30. Transformed cells according to ~~one of~~ claims 26 ~~to 29~~, characterized in that, they contain an increased proportion of the central metabolism metabolites participating in the synthesis of the corresponding amino acid.

31. Transformed cells according to ~~one of~~ claims ~~26 to~~ 30, characterized in that, they contain a reduced proportion of the central metabolism metabolites which do not participate in the synthesis of the corresponding amino acid.

32. The use of a pyruvate-carboxylase gene for increasing the production of amino acids of the aspartate and/or glutamate families by microorganisms.

33. The use according to claim 32, characterized in that, a mutated pyruvate-carboxylase gene which codes for an enzyme with increase pyruvate-carboxylase activity is used.

34. The use according to claim 32 ~~or 33~~, characterized in that, the microorganism producing the corresponding amino acid

is transformed with a gene construct that contains a pyruvate-carboxylase gene.

35. The use according to claim 34, characterized in that, the gene construct additionally contains regulatory gene sequences.

36. The use according to ~~one of~~ claims 32 ~~or 35~~, characterized in that, a pyruvate-carboxylase gene from *Corynebacterium* is used.

37. The use according to ~~one of~~ claims 32 ~~or 36~~, characterized in that, *Corynebacterium* is used as the amino acid-producing microorganism.

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